



SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Coughlin, Shaun
Ishihari, Hiroaki
Connolly, Andrew

(ii) TITLE OF THE INVENTION: Protease Activated Receptor
3 and Uses Thereof

(iii) NUMBER OF SEQUENCES: 23

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: MORRISON & FOERSTER
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(C) CITY: Palo Alto
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94304-1018

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/208,629
(B) FILING DATE: 08-DEC-1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/742,440
(B) FILING DATE: 30-OCT-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Catherine M. Polizzi
(B) REGISTRATION NUMBER: 40,130
(C) REFERENCE/DOCKET NUMBER: 22000-20604.00

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650) 813-5600
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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGACTTTGTA	TACTTAACAA	CATCCTGTAG	CCGGGTCTCA	GGACATCAAG	ATGAAAATCC	60
TTATCTTGGT	TGCAGCTGGG	CTGCTGTTTC	TGCCAGTCAC	TGTTTGCCAA	AGTGGCATAA	120
ATGTTTCAGA	CAACTCAGCA	AAGCCAACCT	TAACTATTAA	GAGTTTAAAT	GGGGGTCCCC	180
AAAATACCTT	TGAAGAATTC	CCACTTTCTG	ACATAGAGGG	CTGGACAGGA	GCCACCACAA	240
CTATAAAAGC	GGAGTGTCCC	GAGGACAGTA	TTTCAACTCT	CCACGTGAAT	AATGCTACCA	300
TAGGATACCT	GAGAAGTTCC	TTAAGTACCC	AAGTGATACC	TGCCATCTAT	ATCCTGCTGT	360
TTGTGGTTGG	TGTACCATCC	AACATCGTGA	CCCTGTGGAA	ACTCTCCTTA	AGGACCAAAT	420
CCATCAGTCT	GGTCATCTTT	CACACCAACC	TGGCCATCGC	AGATCTCCTT	TTCTGTGTCA	480
CACTGCCATT	TAAGATCGCC	TACCATCTCA	ATGGCAACAA	CTGGGTATTT	GGCGAGGTCA	540
TGTGCCGGAT	CACCACGGTC	GTTTTCTACG	GCAACATGTA	CTGCGCTATC	CTGATCCTCA	600
CTTGATGGG	CATCAACCGC	TACCTGGCCA	CGGCTCACCC	TTTCACATAC	CAGAAGCTGC	660
CCAAACGCAG	CTTCTCCTTG	CTCATGTGTG	GCATAGTGTG	GGTCATGGTT	TTCTTATACA	720
TGCTGCCCTT	TGTCATCCTG	AAGCAGGAGT	ACCACCTCGT	CCACTCAGAG	ATCACCACCT	780
GCCACGATGT	CGTCGACGCG	TGCGAGTCCC	CATCATCCTT	CCGATTCTAC	TACTTCGTCT	840
CCTTAGCATT	CTTTGGGTTC	CTCATCCCCT	TTGTGATCAT	CATCTTCTGT	TACACGACTC	900
TCATCCACAA	ACTTAAATCA	AAGGATCGGA	TATGGCTGGG	CTACATCAAG	GCCGTCCTCC	960
TCATCCTTGT	GATTTTCACA	ATTTGCTTTG	CCCCCACCAG	CATCATACTC	GTAATCCACC	1020
ATGCCAACTA	CTACTACCAC	AATACCGACA	GCTTGTACTT	TATGTATCTT	ATTGCTCTGT	1080
GCCTGGGGAG	CCTGAATAGC	TGCCTAGATC	CATTTCCTTTA	CTTTGTCTATG	TCGAAAGTTG	1140
TAGATCAGCT	TAATCCTTAG	TCGGCAATGG	CAAGACCACT	TTAGAGACCA	AGGAGAGATA	1200
TCTGGGAAGA	CATACATGCT	TGGC				1224

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCATATGCTA	ATATTTCTCT	TCAATTACAG	GCATAAATGT	TTCAGACAAC	TCAGCAAAGC	60
CAACCTTAAC	TATTAAGAGT	TTTAATGGGG	GTCCCCAAAA	TACCTTTGAA	GAATTCNNNN	120
NNNTACAACT	CTCCATGTGA	ATAATGCTAC	CATGGGATAC	CTGAGAAGTT	CCTTAAGTAC	180
CAAAGTGATA	CCTGCCATCT	ACATCCTGGT	GTTTGTGATT	GGTGTACCAG	CGAACATCGT	240
GACCCTGTGG	AAACTCTCCT	CAAGGACCAA	ATCCATCTGT	CTGGTCATCT	TTACACCCAA	300
CCTGGCCATC	GCGGATCTCC	TTTTCTGTGT	CACGCTGCCG	TTTAAGATCN	NCCTACCATC	360
TCAATGGCAA	CAACTGGGTA	TTTGCGCAGG	TCATGTGCCG	GATCACCACG	GTCGTTTTCT	420
ACGGCAACAT	GTA CTGCGCT	ANNNTCCTGA	TCCTCACCTG	CATGGGCATC	AACCGCTACC	480
TGGCCACGGC	TCACCCTTTC	ACATACCAGA	AGCTGCCCAA	ACGCAGCTTC	TCCATGCTCA	540
TGTGTGGCAT	GGTGTGGGTC	ATGGTTTTCT	TATACATGCT	GCCCTTTGTC	ATCCNNNAAG	600
CAGGAGTACC	ACCTCGTCCA	CTCCGAGATC	ACCACCTGCC	ACGATGTCGT	CGACGCGTGC	660
GANTCCCCAT	CATCCTTCCG	ATTCTACTAC	TTCGTCTCCT	TAGCATTCTT	TGGGTTCCCTC	720
ATCCCGTTTG	TGATCATCAT	CTTCTGTTAC	ACGACTCTCA	TCCACAAACT	TAAATCAAAA	780
GATCNGATAT	GGCTGGGCTA	CATCAAGGCC	GTCCTCCTCA	TCCTTGTGAA	TTTCACCATC	840
TGCTTCCCCC	CCACCAAGNN	NNNNGATATC	TGGGAAGACG	TACATGCTTG	GCTGACTTGT	900
GCATGGCACC	ATCAGCTCAA	TTTTTAATTT	TTTAATTTTA	ATTTAATTTA	ATTTTATGTT	960
TTTGAGACAG	AGCCTCACTG	TGTAGTCCTG	GCTGGCCTGG	CTGGTTCTCT	ATTTAGACCA	1020
GGTTAGCCTT	GAATCACAG	AGATCTGCCT	GCTTCTGCCT	CCCAAGTGCT	GGGTTCAACC	1080

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 5, 386, 394
- (D) OTHER INFORMATION: Xaa = stop

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Thr Leu Tyr Thr Xaa Gln His Pro Val Ala Gly Ser Gln Asp Ile Lys
 1           5           10           15
Met Lys Ile Leu Ile Leu Val Ala Ala Gly Leu Leu Phe Leu Pro Val
          20           25           30
Thr Val Cys Gln Ser Gly Ile Asn Val Ser Asp Asn Ser Ala Lys Pro
          35           40           45
Thr Leu Thr Ile Lys Ser Phe Asn Gly Gly Pro Gln Asn Thr Phe Glu
 50           55           60
Glu Phe Pro Leu Ser Asp Ile Glu Gly Trp Thr Gly Ala Thr Thr Thr
 65           70           75           80
Ile Lys Ala Glu Cys Pro Glu Asp Ser Ile Ser Thr Leu His Val Asn
          85           90           95
Asn Ala Thr Ile Gly Tyr Leu Arg Ser Ser Leu Ser Thr Gln Val Ile
          100          105          110
Pro Ala Ile Tyr Ile Leu Leu Phe Val Val Gly Val Pro Ser Asn Ile
          115          120          125
Val Thr Leu Trp Lys Leu Ser Leu Arg Thr Lys Ser Ile Ser Leu Val
          130          135          140
Ile Phe His Thr Asn Leu Ala Ile Ala Asp Leu Leu Phe Cys Val Thr
          145          150          155          160
Leu Pro Phe Lys Ile Ala Tyr His Leu Asn Gly Asn Asn Trp Val Phe
          165          170          175
Gly Glu Val Met Cys Arg Ile Thr Thr Val Val Phe Tyr Gly Asn Met
          180          185          190
Tyr Cys Ala Ile Leu Ile Leu Thr Cys Met Gly Ile Asn Arg Tyr Leu
          195          200          205
Ala Thr Ala His Pro Phe Thr Tyr Gln Lys Leu Pro Lys Arg Ser Phe
          210          215          220
Ser Leu Leu Met Cys Gly Ile Val Trp Val Met Val Phe Leu Tyr Met
          225          230          235          240
Leu Pro Phe Val Ile Leu Lys Gln Glu Tyr His Leu Val His Ser Glu
          245          250          255
Ile Thr Thr Cys His Asp Val Val Asp Ala Cys Glu Ser Pro Ser Ser
          260          265          270
Phe Arg Phe Tyr Tyr Phe Val Ser Leu Ala Phe Phe Gly Phe Leu Ile
          275          280          285
Pro Phe Val Ile Ile Ile Phe Cys Tyr Thr Thr Leu Ile His Lys Leu
          290          295          300
Lys Ser Lys Asp Arg Ile Trp Leu Gly Tyr Ile Lys Ala Val Leu Leu

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305		310		315		320
Ile	Leu	Val	Ile	Phe	Thr	Ile
		325		330		335
Val	Ile	His	His	Ala	Asn	Tyr
		340		345		350
Phe	Met	Tyr	Leu	Ile	Ala	Leu
		355		360		365
Asp	Pro	Phe	Leu	Tyr	Phe	Val
		370		375		380
Pro	Xaa	Ser	Ala	Met	Ala	Arg
		385		390		395
Trp	Glu	Asp	Ile	His	Ala	Trp
						400
						405

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGCTCCATGA	TTTTACAGAT	TTCATAACGT	TTAAGAGACG	GGACTCAGGT	CATCAAAATG	60
AAAGCCCTCA	TCTTTGCAGC	TGCTGGCCTC	CTGCTTCTGT	TGCCCACCTT	TTGTCAGAGT	120
GGCATGGAAA	ATGATACAAA	CAACTTGGCA	AAGCCAACCT	TACCCATTAA	GACCTTTCGT	180
GGAGCTCCCC	CAAATTCTTT	TGAAGAGTTC	CCCTTTTCTG	CCTTGGAAGG	CTGGACAGGA	240
GCCACGATTA	CTGTAAAAAT	TAAGTGCCCT	GAAGAAAGTG	CTTCACATCT	CCATGTGAAA	300
AATGCTACCA	TGGGGTACCT	GACCAGCTCC	TTAAGTACTA	AACTGATACC	TGCCATCTAC	360
CTCCTGGTGT	TTGTAGTTGG	TGTCCCGGCC	AATGCTGTGA	CCCTGTGGAT	GCTTTTCTTC	420
AGGACCAGAT	CCATCTGTAC	CACTGTATTC	TACACCAACC	TGGCCATTGC	AGATTTTCTT	480
TTTTGTGTTA	CATTGCCCTT	TAAGATAGTC	TATCATCTCA	ATGGGAACAA	CTGGGTATTT	540
GGAGAGGTCC	TGTGCCGGGC	CACCACAGTC	ATCTTCTATG	GCAACATGTA	CTGCTCCATT	600
CTGCTCCTTG	CCTGCATCAG	CATCAACCGC	TACCTGGCCA	TCGTCCATCC	TTTCACCTAC	660
CGGGGCCTGC	CCAAGCACAC	CTATGCCTTG	GTAACATGTG	GACTGGTGTG	GGCAACAGTT	720
TTCTTATATA	TGCTGCCATT	TTTCATACTG	AAGCAGGAAT	ATTATCTTGT	TCAGCCAGAC	780
ATCACCACT	GCCATGATGT	TCACAACACT	TGCGAGTCCT	CATCTCCCTT	CCAACCTCTAT	840
TACTTCATCT	CCTTGGCATT	CTTTGGATTG	TTAATTCCAT	TTGTGCTTAT	CATCTACTGC	900
TATGCAGCCA	TCATCCGGAC	ACTTAATGCA	TACGATCATA	GATGGTTGTG	GTATGTTAAG	960
GCGAGTCTCC	TCATCCTTGT	GATTTTTTACC	ATTTGCTTTG	CTCCAAGCAA	TATTATTCTT	1020
ATTATTACAC	ATGCTAACTA	CTACTACAAC	AACACTGATG	GCTTATATTT	TATATATCTC	1080
ATAGCTTTGT	GCCTGGGTAG	TCTTAATAGT	TGCTTAGATC	CATTCCCTTA	TTTTCTCATG	1140
TCAAAAACCA	GAAATCACTC	CACTGCTTAC	CTTACAAAAT	AGTGAAATGA	TCTTAGAGAA	1200
CAAGGACAGC	CATCACAGAG	AACG				1224

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACAGGCATGG	AAAATGATAC	AAACAACTTG	GCAAAGCCAA	CCTTACCCAT	TAAGACCTTT	60
CGTGGAGCTC	CCCCAAATTC	TTTTGAAGAG	TTCCCCTTTT	CTGCCTTGGA	AGGCTGGACA	120
GGAGCCACGA	TTACTGTAAA	AATTAAGTGC	CCTGAAGAAA	GTGCTTCACA	TCTCCATGTG	180
AAAAATGCTA	CCATGGGGTA	CCTGACCAGC	TCCTTAAGTA	CTAAACTGAT	ACCTGCCATC	240
TACCTCCTGG	TGTTTGTAGT	TGGTGTCCCG	GCCAATGCTG	TGACCCTGTG	GATGCTTTTC	300
TTCAGGACCA	GATCCATCTG	TACCACTGTA	TTCTACACCA	ACCTGGCCAT	TGCAGATTTT	360
CTTTTTTGTG	TTACATTGCC	CTTTAAGATA	GCTTATCATC	TCAATGGGAA	CAACTGGGTA	420
TTTGGAGAGG	TCCTGTGCCG	GGCCACCACA	GTCATCTTCT	ATGGCAACAT	GTA CTGCTCC	480
ATTCTGCTCC	TTGCCTGCAT	CAGCATCAAC	CGCTACCTGG	CCATCGTCCA	TCCTTTTACC	540
TACCGGGGCC	TGCCCCAAGCA	CACCTATGCC	TTGGTAACAT	GTGGACTGGT	GTGGGCAACA	600
GTTTTCTTAT	ATATGCTGCC	ATTTTTCATA	CTGAAGCAGG	AATATTATCT	TGTTTCAGCCA	660
GACATCACCA	CCTGCCATGA	TGTTCAACAAC	ACTTGCGAGT	CCTCATCTCC	CTTCCAACTC	720
TATTACTTCA	TCTCCTTGGC	ATTCTTTGGA	TTCTTAATTC	CATTTGTGCT	TATCATCTAC	780
TGCTATGCAG	CCATCATCCG	GACACTTAAT	GCATACGATC	ATAGATGGTT	GTGGTATGTT	840
AAGGCGAGTC	TCCTCATCCT	TGTGATTTTT	ACCATTTGCT	TTGCTCCAAG	CAATATTATT	900
CTTATTATTC	ACCATGCTAA	CTACTACTAC	AACAACACTG	ATGGCTTATA	TTTTATATAT	960
CTCATAGCTT	TGTGCCTGGG	TAGTCTTAAT	AGTTGCTTAG	ATCCATTCCT	TTATTTTCTC	1020
ATGTCAAAAA	CCAGAAATCA	CTCCACTGCT	TACCTTACAA	AATAGTGAAA	TGATCTTAGA	1080
GAACAAGGAC	AGCCATCACA	GA				1102

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 9, 394, 395
- (D) OTHER INFORMATION: Xaa = stop

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Cys	Ser	Met	Ile	Leu	Gln	Ile	Ser	Xaa	Arg	Leu	Arg	Asp	Gly	Thr	Gln
1				5				10						15	
Val	Ile	Lys	Met	Lys	Ala	Leu	Ile	Phe	Ala	Ala	Ala	Gly	Leu	Leu	Leu
			20					25					30		
Leu	Leu	Pro	Thr	Phe	Cys	Gln	Ser	Gly	Met	Glu	Asn	Asp	Thr	Asn	Asn
			35				40					45			
Leu	Ala	Lys	Pro	Thr	Leu	Pro	Ile	Lys	Thr	Phe	Arg	Gly	Ala	Pro	Pro
			50			55					60				
Asn	Ser	Phe	Glu	Glu	Phe	Pro	Phe	Ser	Ala	Leu	Glu	Gly	Trp	Thr	Gly
65					70				75					80	
Ala	Thr	Ile	Thr	Val	Lys	Ile	Lys	Cys	Pro	Glu	Glu	Ser	Ala	Ser	His
				85				90						95	
Leu	His	Val	Lys	Asn	Ala	Thr	Met	Gly	Tyr	Leu	Thr	Ser	Ser	Leu	Ser
			100				105						110		
Thr	Lys	Leu	Ile	Pro	Ala	Ile	Tyr	Leu	Leu	Val	Phe	Val	Val	Gly	Val
			115				120						125		
Pro	Ala	Asn	Ala	Val	Thr	Leu	Trp	Met	Leu	Phe	Phe	Arg	Thr	Arg	Ser
			130			135						140			
Ile	Cys	Thr	Thr	Val	Phe	Tyr	Thr	Asn	Leu	Ala	Ile	Ala	Asp	Phe	Leu

145		150		155		160
Phe Cys Val Thr	Leu Pro Phe Lys Ile	Ala Tyr His Leu Asn Gly Asn				
	165	170	175			
Asn Trp Val Phe	Gly Glu Val Leu Cys Arg Ala Thr Thr	Val Ile Phe				
	180	185	190			
Tyr Gly Asn Met	Tyr Cys Ser Ile Leu Leu Leu Ala Cys	Ile Ser Ile				
	195	200	205			
Asn Arg Tyr Leu	Ala Ile Val His Pro Phe Thr Tyr Arg Gly Leu Pro					
	210	215	220			
Lys His Thr Tyr	Ala Leu Val Thr Cys Gly Leu Val Trp Ala Thr Val					
225	230	235	240			
Phe Leu Tyr Met	Leu Pro Phe Phe Ile Leu Lys Gln Glu Tyr Tyr Leu					
	245	250	255			
Val Gln Pro Asp	Ile Thr Thr Cys His Asp Val His Asn Thr Cys Glu					
	260	265	270			
Ser Ser Ser Pro	Phe Gln Leu Tyr Tyr Phe Ile Ser Leu Ala Phe Phe					
	275	280	285			
Gly Phe Leu Ile	Pro Phe Val Leu Ile Ile Tyr Cys Tyr Ala Ala Ile					
	290	295	300			
Ile Arg Thr Leu	Asn Ala Tyr Asp His Arg Trp Leu Trp Tyr Val Lys					
305	310	315	320			
Ala Ser Leu Leu	Ile Leu Val Ile Phe Thr Ile Cys Phe Ala Pro Ser					
	325	330	335			
Asn Ile Ile Leu	Ile Ile His His Ala Asn Tyr Tyr Tyr Asn Asn Thr					
	340	345	350			
Asp Gly Leu Tyr	Phe Ile Tyr Leu Ile Ala Leu Cys Leu Gly Ser Leu					
	355	360	365			
Asn Ser Cys Leu	Asp Pro Phe Leu Tyr Phe Leu Met Ser Lys Thr Arg					
	370	375	380			
Asn His Ser Thr	Ala Tyr Leu Thr Lys Xaa Xaa Asn Asp Leu Arg Glu					
385	390	395	400			
Gln Gly Gln Pro	Ser Gln Arg Thr					
	405					

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Gly Pro Arg Arg	Leu Leu Leu Val	Ala Ala Cys Phe Ser	Leu Cys
1	5	10	15
Gly Pro Leu Leu Ser	Ala Arg Thr Arg	Ala Arg Arg Pro	Glu Ser Lys
	20	25	30
Ala Thr Asn Ala Thr	Leu Asp Pro Arg Ser	Phe Leu Leu Arg	Asn Pro
	35	40	45
Asn Asp Lys Tyr Glu	Pro Phe Trp Glu Asp	Glu Glu Lys Asn	Glu Ser
	50	55	60
Gly Leu Thr Glu Tyr	Arg Leu Val Ser Ile	Asn Lys Ser Ser	Pro Leu
65	70	75	80
Gln Lys Gln Leu Pro	Ala Phe Ile Ser Glu Asp	Ala Ser Gly Tyr	Leu

				85				90					95				
Thr	Ser	Ser	Trp	Leu	Thr	Leu	Phe	Val	Pro	Ser	Val	Tyr	Thr	Gly	Val		
			100					105					110				
Phe	Val	Val	Ser	Leu	Pro	Leu	Asn	Ile	Met	Ala	Ile	Val	Val	Phe	Ile		
		115					120					125					
Leu	Lys	Met	Lys	Val	Lys	Lys	Pro	Ala	Val	Val	Tyr	Met	Leu	His	Leu		
	130					135					140						
Ala	Thr	Ala	Asp	Val	Leu	Phe	Val	Ser	Val	Leu	Pro	Phe	Lys	Ile	Ser		
145					150					155					160		
Tyr	Tyr	Phe	Ser	Gly	Ser	Asp	Trp	Gln	Phe	Gly	Ser	Glu	Leu	Cys	Arg		
			165					170						175			
Phe	Val	Thr	Ala	Ala	Phe	Tyr	Cys	Asn	Met	Tyr	Ala	Ser	Ile	Leu	Leu		
		180						185					190				
Met	Thr	Val	Ile	Ser	Ile	Asp	Arg	Phe	Leu	Ala	Val	Val	Tyr	Pro	Met		
	195						200					205					
Gln	Ser	Leu	Ser	Trp	Arg	Thr	Leu	Gly	Arg	Ala	Ser	Phe	Thr	Cys	Leu		
	210					215					220						
Ala	Ile	Trp	Ala	Leu	Ala	Ile	Ala	Gly	Val	Val	Pro	Leu	Val	Leu	Lys		
225				230					235						240		
Glu	Gln	Thr	Ile	Gln	Val	Pro	Gly	Leu	Asn	Ile	Thr	Thr	Cys	His	Asp		
			245					250						255			
Val	Leu	Asn	Glu	Thr	Leu	Leu	Glu	Gly	Tyr	Tyr	Ala	Tyr	Tyr	Phe	Ser		
		260					265						270				
Ala	Phe	Ser	Ala	Val	Phe	Phe	Phe	Val	Pro	Leu	Ile	Ile	Ser	Thr	Val		
	275						280					285					
Cys	Tyr	Val	Ser	Ile	Ile	Arg	Cys	Leu	Ser	Ser	Ser	Ala	Val	Ala	Asn		
	290					295				300							
Arg	Ser	Lys	Lys	Ser	Arg	Ala	Leu	Phe	Leu	Ser	Ala	Ala	Val	Phe	Cys		
305					310					315					320		
Ile	Phe	Ile	Ile	Cys	Phe	Gly	Pro	Thr	Asn	Val	Leu	Leu	Ile	Ala	His		
			325					330						335			
Tyr	Ser	Phe	Leu	Ser	His	Thr	Ser	Thr	Thr	Glu	Ala	Ala	Tyr	Phe	Ala		
		340					345						350				
Tyr	Leu	Leu	Cys	Val	Cys	Val	Ser	Ser	Ile	Ser	Ser	Cys	Ile	Asp	Pro		
	355					360						365					
Leu	Ile	Tyr	Tyr	Tyr	Ala	Ser	Ser	Glu	Cys	Gln	Arg	Tyr	Val	Tyr	Ser		
370					375					380							
Ile	Leu	Cys	Cys	Lys	Glu	Ser	Ser	Asp	Pro	Ser	Ser	Tyr	Asn	Ser	Ser		
385				390					395					400			
Gly	Gln	Leu	Met	Ala	Ser	Lys	Met	Asp	Thr	Cys	Ser	Ser	Asn	Leu	Asn		
			405					410						415			
Asn	Ser	Ile	Tyr	Lys	Lys	Leu	Leu	Thr									
		420					425										

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Arg Ser Pro Ser Ala Ala Trp Leu Leu Gly Ala Ala Ile Leu Leu

1	5	10	15
Ala	Ala Ser Leu Ser Cys Ser Gly Thr Ile Gln Gly Thr Asn Arg Ser		
	20	25	30
Ser Lys Gly Arg Ser Leu Ile Gly Lys Val Asp Gly Thr Ser His Val			
	35	40	45
Thr Gly Lys Gly Val Thr Val Glu Thr Val Phe Ser Val Asp Glu Phe			
	50	55	60
Ser Ala Ser Val Leu Thr Gly Lys Leu Thr Thr Val Phe Leu Pro Ile			
65	70	75	80
Val Tyr Thr Ile Val Phe Val Val Gly Leu Pro Ser Asn Gly Met Ala			
	85	90	95
Leu Trp Val Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val Ile			
	100	105	110
Tyr Met Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp Phe			
	115	120	125
Pro Leu Lys Ile Ala Tyr His Ile His Gly Asn Asn Trp Ile Tyr Gly			
	130	135	140
Glu Ala Leu Cys Asn Val Leu Ile Gly Phe Phe Tyr Gly Asn Met Tyr			
145	150	155	160
Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp Val			
	165	170	175
Ile Val Asn Pro Met Gly His Ser Arg Lys Lys Ala Asn Ile Ala Ile			
	180	185	190
Gly Ile Ser Leu Ala Ile Trp Leu Leu Ile Leu Leu Val Thr Ile Pro			
	195	200	205
Leu Tyr Val Val Lys Gln Thr Ile Phe Ile Pro Ala Leu Asn Ile Thr			
	210	215	220
Thr Cys His Asp Val Leu Pro Glu Gln Leu Leu Val Gly Asp Pro Phe			
225	230	235	240
Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala Phe Leu Thr Ala			
	245	250	255
Ser Ala Tyr Val Leu Met Ile Arg Met Leu Arg Ser Ser Ala Met Asp			
	260	265	270
Glu Asn Ser Glu Lys Lys Arg Lys Arg Ala Ile Lys Leu Ile Val Thr			
	275	280	285
Val Leu Ala Met Tyr Leu Ile Cys Phe Thr Pro Ser Asn Leu Leu Leu			
	290	295	300
Val Val His Tyr Phe Leu Ile Lys Ser Gln Gly Gln Ser His Val Tyr			
305	310	315	320
Ala Leu Tyr Ile Val Ala Leu Cys Leu Ser Thr Leu Asn Ser Cys Ile			
	325	330	335
Asp Pro Phe Val Tyr Tyr Phe Val Ser His Asp Phe Arg Asp His Ala			
	340	345	350
Lys Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Lys Gln Met Gln			
	355	360	365
Val Ser Leu Thr Ser Lys Lys His Ser Arg Lys Ser Ser Ser Tyr Ser			
	370	375	380
Ser Ser Ser Thr Thr Val Lys Thr Ser Tyr			
385	390		

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Phe Glu Glu Ile Pro Glu Glu Tyr Leu Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...29
- (D) OTHER INFORMATION: N=Inosine at residues 3, 12, 18, 21, and 24

- (A) NAME/KEY: Other
- (B) LOCATION: 22...27
- (D) OTHER INFORMATION: N=A or C or G or T at residues 22 and 27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTNTACATGC TNMACYTNGC NNTNGCNGA

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 6...21
- (D) OTHER INFORMATION: N=Inosine at residue 6, 9, 12, 15, and 21

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 24
- (D) OTHER INFORMATION: N=A or C or G or T at residue 24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGATANACNA CNGCNADRWA NCKBTC

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asp Tyr Lys Asp Asp Asp
1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Asp Ser Lys Gly Ser Ser Gln Lys Gly Ser Arg Leu Leu Leu Leu
1 5 10 15
Leu Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr
20 25 30
Lys Asp Asp Asp Asp Val Glu
35

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Phe Glu Glu Phe Pro
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Leu Thr Pro Lys

1

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Phe Arg Gly Ala Pro

1

5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Thr Phe Arg Gly Ala Pro Pro Asn Ser

1

5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Pro Ile Lys Thr Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu

1

5

10

15

Phe Pro Phe Ser Ala Leu Glu

20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Leu Pro Ile Lys Pro Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu
1 5 10 15
Phe Pro Phe Ser Ala Leu Glu
20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Leu Pro Ile Xaa Thr Pro Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu
1 5 10 15
Glu Phe Pro Phe Ser Ala Leu Glu
20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Xaa Pro Arg Pro Phe Arg Gly Ala Pro Pro Asn Ser Phe Glu Glu Phe
1 5 10 15
Pro Phe Ser Ala Leu Glu
20

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Leu Pro Ile Lys

1

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Thr Phe Arg Gly Ala Pro Pro Asn Ser

1

5

*Sub
B1
concluded*